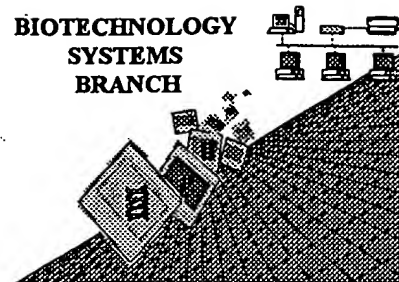


Saunders
RAW SEQUENCE LISTING
ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/121,017

Art Unit / Team No. : 1644

Date Processed by STIC: 12/17/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/12/07

TN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- ___ **Wrapped Nucleics** The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- ___ **Wrapped Aminos** The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- ___ **Incorrect Line Length** The rules require that a line not exceed 72 characters in length. This includes spaces.
- ___ **Misaligned Amino Acid Numbering** The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- ___ **Non-ASCII** This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- ___ **Variable Length** Sequence(s) ___ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- ___ **PatentIn ver. 2.0 "bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- ___ **Skipped Sequences (OLD RULES)** Sequence(s) ___ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- ___ **Skipped Sequences (NEW RULES)** Sequence(s) ___ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- ___ **Use of n's or Xaa's (NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- ___ **Use of <213>Organism (NEW RULES)** Sequence(s) _____ are missing this mandatory field or its response.
- ___ **Use of <220>Feature (NEW RULES)** Sequence(s) 135 (maybe more) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- ___ **PatentIn ver. 2.0 "bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/121,017

DATE: 12/17/1999
TIME: 16:20:58

Input Set: I121017.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

Does Not Comply
Corrected Diskette Needed

1 <110> APPLICANT: Imamura, Toru
2 Asada, Masahiro
3 Oka, Syuichi
4 Suzuki, Masashi
5 Yoneda, Atsuko
6 Ota, Keiko
7 Oda, Yuko
8 Miyakawa, Kazuko
9 Orikasa, Noriko
10 Asada, Chie
11 Kojima, Tetsuhito
12 <120> TITLE OF INVENTION: HEPARIN-BINDING PROTEINS MODIFIED WITH SUGAR CHAINS,
13 METHOD OF PRODUCING THE SAME AND PHARMACEUTICAL
14 COMPOSITIONS CONTAINING THE SAME
15 <130> FILE REFERENCE: PH-559US
16 <140> CURRENT APPLICATION NUMBER: US/09/121,017
17 <141> CURRENT FILING DATE: 1998-07-23
18 <150> EARLIER APPLICATION NUMBER: 307721/1997
19 <151> EARLIER FILING DATE: 1997-11-10
20 <160> NUMBER OF SEQ ID NOS: 30
21 <170> SOFTWARE: PatentIn Ver. 2.0
22 <210> SEQ ID NO 1
23 <211> LENGTH: 221
24 <212> TYPE: PRT
25 <213> ORGANISM: Artificial Sequence
26 <400> SEQUENCE: 1
27 Met Ala Pro Ala Arg Leu Phe Ala Leu Leu Phe Phe Val Gly Gly
28 1 5 10 15
29 Val Ala Glu Ser Ile Arg Glu Thr Glu Val Ile Asp Pro Gln Asp Leu
30 20 25 30
31 Leu Glu Gly Arg Tyr Phe Ser Gly Ala Leu Pro Asp Asp Glu Asp Val
32 35 40 45
33 Val Gly Pro Gly Gln Glu Ser Asp Asp Phe Glu Leu Ser Gly Ser Gly
34 50 55 60
35 Asp Leu Asp Asp Leu Glu Asp Ser Met Ile Gly Pro Glu Val Val His
36 65 70 75 80
37 Pro Leu Val Pro Leu Asp Ala Asn Tyr Lys Lys Pro Lys Leu Leu Tyr
38 85 90 95
39 Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val
40 100 105 110
41 Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser
42 115 120 125
43 Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln
44 130 135 140

see item 12 on Ena summary sheet

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RAW SEQUENCE LISTING
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45      Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro
46      145                      150                      155                      160
47      Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn
48                      165                      170                      175
49      Thr Tyr Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu
50                      180                      185                      190
51      Lys Lys Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln
52                      195                      200                      205
53      Lys Ala Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
54      210                      215                      220
55      <210> SEQ ID NO 2
56      <211> LENGTH: 663
57      <212> TYPE: DNA
58      <213> ORGANISM: Artificial Sequence
59      <220> FEATURE:
60      <223> OTHER INFORMATION: Description of Artificial Sequence: fusion of
61      sequence for a part of human rydocal and a part of human fibroblast
62      growth factor 1
63      <220> FEATURE:
64      <221> NAME/KEY: CDS
65      <222> LOCATION: (1)..(663)
66      <400> SEQUENCE: 2
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68      Met Ala Pro Ala Arg Leu Phe Ala Leu Leu Leu Phe Phe Val Gly Gly
69      1                      5                      10                      15
70      gtc gcc gag tcg atc cga gag act gag gtc atc gac ccc cag gac ctc      96
71      Val Ala Glu Ser Ile Arg Glu Thr Glu Val Ile Asp Pro Gln Asp Leu
72                      20                      25                      30
73      cta gaa ggc cga tac ttc tcc gga gcc cta cca gac gat gag gat gta      144
74      Leu Glu Gly Arg Tyr Phe Ser Gly Ala Leu Pro Asp Asp Glu Asp Val
75                      35                      40                      45
76      gtg ggg ccc ggg cag gaa tct gat gac ttt gag ctg tct ggc tct gga      192
77      Val Gly Pro Gly Gln Glu Ser Asp Asp Phe Glu Leu Ser Gly Ser Gly
78      50                      55                      60
79      gat ctg gat gac ttg gaa gac tcc atg atc ggc cct gaa gtt gtc cat      240
80      Asp Leu Asp Asp Leu Glu Asp Ser Met Ile Gly Pro Glu Val Val His
81      65                      70                      75                      80
82      ccc ttg gtg cct cta gat gct aat tac aag aag ccc aaa ctc ctc tac      288
83      Pro Leu Val Pro Leu Asp Ala Asn Tyr Lys Lys Pro Lys Leu Leu Tyr
84                      85                      90                      95
85      tgt agc aac ggg ggc cac ttc ctg agg atc ctt ccg gat ggc aca gtg      336
86      Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val
87      100                      105                      110
88      gat ggg aca agg gac agg agc gac cag cac att cag ctg cag ctc agt      384
89      Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser
90      115                      120                      125
91      gcg gaa agc gtg ggg gag gtg tat ata aag agt acc gag act ggc cag      432
92      Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln
93      130                      135                      140
94      tac ttg gcc atg gac acc gac ggg ctt tta tac ggc tca cag aca cca      480

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RAW SEQUENCE LISTING
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DATE: 12/17/1999
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Input Set: I121017.RAW

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105      Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro
106      145                      150                      155                      160
107      aat gag gaa tgt ttg ttc ctg gaa agg ctg gag gag aac cat tac aac      528
108      Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn
109      165                      170                      175
110      acc tat ata tcc aag aag cat gca gag aag aat tgg ttt gtt ggc ctc      576
111      Thr Tyr Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu
112      180                      185                      190
113      aag aag aat ggg agc tgc aaa cgc ggt cct cgg act cac tat ggc cag      624
114      Lys Lys Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln
115      195                      200                      205
116      aaa gca atc ttg ttt ctc ccc ctg cca gtc tct tct gat      663
117      Lys Ala Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
118      210                      215                      220

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109 <210> SEQ ID NO 3

110 <211> LENGTH: 175

111 <212> TYPE: PRT

112 <213> ORGANISM: Artificial Sequence

113 <400> SEQUENCE: 3

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114      Met Ser Arg Gly Ala Gly Arg Val Gln Gly Thr Leu Gln Ala Leu Val
115      1                      5                      10                      15
116      Phe Leu Gly Val Leu Val Gly Met Val Val Pro Ser Pro Ala Gly Ala
117      20                      25                      30
118      Arg Ala Asn Gly Thr Leu Leu Asp Ala Asn Tyr Lys Lys Pro Lys Leu
119      35                      40                      45
120      Leu Tyr Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly
121      50                      55                      60
122      Thr Val Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln
123      65                      70                      75                      80
124      Leu Ser Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr
125      85                      90                      95
126      Gly Gln Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln
127      100                     105                     110
128      Thr Pro Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His
129      115                     120                     125
130      Tyr Asn Thr Tyr Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val
131      130                     135                     140
132      Gly Leu Lys Lys Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr
133      145                     150                     155                     160
134      Gly Gln Lys Ala Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
135      165                     170                     175

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136 <210> SEQ ID NO 4

137 <211> LENGTH: 525

138 <212> TYPE: DNA

139 <213> ORGANISM: Artificial Sequence

140 <220> FEATURE:

141 <223> OTHER INFORMATION: Description of Artificial Sequence: fusion of
 142 sequence for a part of mouse fibroblast growth factor 6 and
 143 a part of human fibroblast growth factor 1

144 <220> FEATURE:

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146 <222> LOCATION: (1)..(525)
147 <400> SEQUENCE: 4
148   atg tcc cgg gga gca gga cgt gtt cag ggc acg ctg cag gct ctc gtc   48
149   Met Ser Arg Gly Ala Gly Arg Val Gln Gly Thr Leu Gln Ala Leu Val
150       1             5             10             15
151   ttc tta ggc gtc cta gtg ggc atg gtg gtc ccc tca cct gcc ggc gcc   96
152   Phe Leu Gly Val Leu Val Gly Met Val Val Pro Ser Pro Ala Gly Ala
153       20             25             30
154   cgc gcc aac ggc acg cta ctg gac gct aat tac aag aag ccc aaa ctc   144
155   Arg Ala Asn Gly Thr Leu Leu Asp Ala Asn Tyr Lys Lys Pro Lys Leu
156       35             40             45
157   ctc tac tgt agc aac ggg ggc cac ttc ctg agg atc ctt ccg gat ggc   192
158   Leu Tyr Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly
159       50             55             60
160   aca gtg gat ggg aca agg gac agg agc gac cag cac att cag ctg cag   240
161   Thr Val Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln
162       65             70             75             80
163   ctc agt gcg gaa agc gtg ggg gag gtg tat ata aag agt acc gag act   288
164   Leu Ser Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr
165       85             90             95
166   ggc cag tac ttg gcc atg gac acc gac ggg ctt tta tac ggc tca cag   336
167   Gly Gln Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln
168       100            105            110
169   aca cca aat gag gaa tgt ttg ttc ctg gaa agg ctg gag gag aac cat   384
170   Thr Pro Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His
171       115            120            125
172   tac aac acc tat ata tcc aag aag cat gca gag aag aat tgg ttt gtt   432
173   Tyr Asn Thr Tyr Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val
174       130            135            140
175   ggc ctc aag aag aat ggg agc tgc aaa cgc ggt cct cgg act cac tat   480
176   Gly Leu Lys Lys Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr
177       145            150            155            160
178   ggc cag aaa gca atc ttg ttt ctc ccc ctg cca gtc tct tct gat   525
179   Gly Gln Lys Ala Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
180       165            170            175
181 <210> SEQ ID NO 5
182 <211> LENGTH: 181
183 <212> TYPE: PRT
184 <213> ORGANISM: Artificial Sequence
185 <400> SEQUENCE: 5
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187       1             5             10             15
188   Phe Leu Gly Val Leu Val Gly Met Val Val Pro Ser Pro Ala Gly Ala
189       20             25             30
190   Arg Ala Gln Gly Thr Leu Leu Asp Ala Asn Tyr Lys Lys Pro Lys Leu
191       35             40             45
192   Leu Tyr Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly
193       50             55             60
194   Thr Val Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln

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195      65      70      75      80
196      Leu Ser Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr
197      85      90      95
198      Gly Gln Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln
199      100      105      110
200      Thr Pro Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Ala Ala
201      115      120      125
202      Thr Pro Ala Pro Asn His Tyr Asn Thr Tyr Ile Ser Lys Lys His Ala
203      130      135      140
204      Glu Lys Asn Trp Phe Val Gly Leu Lys Lys Asn Gly Ser Cys Lys Arg
205      145      150      155      160
206      Gly Pro Arg Thr His Tyr Gly Gln Lys Ala Ile Leu Phe Leu Pro Leu
207      165      170      175
208      Pro Val Ser Ser Asp
209      180
210      <210> SEQ ID NO 6
211      <211> LENGTH: 543
212      <212> TYPE: DNA
213      <213> ORGANISM: Artificial Sequence
214      <220> FEATURE:
215      <223> OTHER INFORMATION: Description of Artificial Sequence: fusion of
216      sequence for a part of mouse fibroblast growth factor 6,
217      a part of human fibroblast growth factor 1 and an artificial
218      sequence
219      <220> FEATURE:
220      <221> NAME/KEY: CDS
221      <222> LOCATION: (1)..(543)
222      <400> SEQUENCE: 6
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224      Met Ser Arg Gly Ala Gly Arg Val Gln Gly Thr Leu Gln Ala Leu Val
225      1      5      10      15
226      ttc tta ggc gtc cta gtg ggc atg gtg gtg ccc tca cct gcc ggc gcc      96
227      Phe Leu Gly Val Leu Val Gly Met Val Val Pro Ser Pro Ala Gly Ala
228      20      25      30
229      cgc gcc caa ggc acg cta ctg gac gct aat tac aag aag ccc aaa ctc      144
230      Arg Ala Gln Gly Thr Leu Leu Asp Ala Asn Tyr Lys Lys Pro Lys Leu
231      35      40      45
232      ctc tac tgt agc aac ggg ggc cac ttc ctg agg atc ctt ccg gat ggc      192
233      Leu Tyr Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly
234      50      55      60
235      aca gtg gat ggg aca agg gac agg agc gac cag cac att cag ctg cag      240
236      Thr Val Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln
237      65      70      75      80
238      ctc agt gcg gaa agc gtg ggg gag gtg tat ata aag agt acc gag act      288
239      Leu Ser Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr
240      85      90      95
241      ggc cag tac ttg gcc atg gac acc gac ggg ctt tta tac ggc tca cag      336
242      Gly Gln Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln
243      100      105      110
244      aca cca aat gag gaa tgt ttg ttc ctg gaa agg ctg gag gag gct gct      384

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VERIFICATION SUMMARY
PATENT APPLICATION US/09/121,017

DATE: 12/17/1999
TIME: 16:20:58

Input Set: I121017.RAW

Line ? Error/Warning

Original Text
